

RAW SEQUENCE LISTING

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Application Serial Number: 10/784,513
Source: IFWJ
Date Processed by STIC: 3/20/2006

ENTERED

RAW SEQUENCE LISTING
PATENT APPLICATION US/10/784,513DATE: 03/20/2006
TIME: 12:29:15

INPUT SET: S30786.raw

<p>This Raw Listing contains the General Information Section and up to the first 5 pages.</p>
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1 SEQUENCE LISTING
2
3 (1) General Information:
4
5 (i) APPLICANT: Gorski, David H.
6 Walsh, Kenneth
7
8 (ii) TITLE OF INVENTION: Growth Arrest Homeobox Gene
9
10 (iii) NUMBER OF SEQUENCES: 19
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: Calfee, Halter, and Griswold
14 (B) STREET: 800 Superior Avenue
15 (C) CITY: Cleveland
16 (D) STATE: Ohio
17 (E) COUNTRY: U.S.A.
18 (F) ZIP: 44114-2688
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER:US/10/784,513
28 (B) FILING DATE: 23-FEB-2004
29 (vii) PRIOR APPLICATION DATA:
30 (A) APPLICATION NUMBER:US/08/203,532
31 (B) FILING DATE: 24-FEB-1994
32 (C) CLASSIFICATION:435
33
34 (viii) ATTORNEY/AGENT INFORMATION:
35 (A) NAME: Golrick, Mary E.
36 (B) REGISTRATION NUMBER: 34829
37 (C) REFERENCE/DOCKET NUMBER: 22311/00114
38
39 (ix) TELECOMMUNICATION INFORMATION:
40 (A) TELEPHONE: (216) 622-8200
41 (B) TELEFAX: (216) 241-0816
42 (C) TELEX: 980499
43
44
45 (2) INFORMATION FOR SEQ ID NO:1:
46

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47      (i) SEQUENCE CHARACTERISTICS:
48          (A) LENGTH: 2244 base pairs
49          (B) TYPE: nucleic acid
50          (C) STRANDEDNESS: both
51          (D) TOPOLOGY: linear
52
53      (ii) MOLECULE TYPE: cDNA
54
55      (iii) HYPOTHETICAL: NO
56
57      (iv) ANTI-SENSE: NO
58
59
60      (ix) FEATURE:
61          (A) NAME/KEY: CDS
62          (B) LOCATION: 197..1108
63
64
65      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
66
67      GTCAAGTGT TATACGTGCA GGAGACTGGC CGCTCGGCTC AGGACTGGGA TTAGCGGGCT      60
68
69      CTGCTCAAAC CCGCGCGGCT TTTACATTAG GAGTGAGTGG GGGAGAGTCC TAGGATTTCT      120
70
71      AGTGAAAAGT GACAGCGCTT GGTGGACTTT GGGACCTTCG TGAAGTCTTC TGCTTGAAG      180
72
73      CTGAGACTTG CATGCC ATG GAA CAC CCC CTC TTT GGC TGC CTG CGC AGC      229
74          Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser
75          1 5 10
76
77      CCC CAC GCC ACA GCG CAA GGC TTG CAC CCC TTC TCG CAG TCT TCT CTG      277
78      Pro His Ala Thr Ala Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu
79          15 20 25
80
81      GCC CTC CAT GGA AGA TCT GAC CAC ATG TCC TAC CCC GAA CTC TCC ACA      325
82      Ala Leu His Gly Arg Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr
83          30 35 40
84
85      TCT TCC TCG TCT TGC ATA ATC GCG GGA TAC CCC AAT GAG GAG GGC ATG      373
86      Ser Ser Ser Ser Cys Ile Ile Ala Gly Tyr Pro Asn Glu Glu Gly Met
87          45 50 55
88
89      TTT GCC AGC CAG CAT CAC AGG GGG CAC CAC CAC CAC CAC CAC CAC CAC      421
90      Phe Ala Ser Gln His His Arg Gly His His His His His His His His
91          60 65 70 75
92
93      CAT CAC CAC CAC CAG CAG CAG CAG CAC CAG GCT CTG CAA AGC AAC TGG      469
94      His His His His Gln Gln Gln Gln His Gln Ala Leu Gln Ser Asn Trp
95          80 85 90
96
97      CAC CTC CCG CAG ATG TCC TCC CCG CCA AGC GCG GCC CGG CAC AGC CTT      517
98      His Leu Pro Gln Met Ser Ser Pro Pro Ser Ala Ala Arg His Ser Leu
99          95 100 105

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102	Cys	Leu	Gln	Pro	Asp	Ser	Gly	Gly	Pro	Pro	Glu	Leu	Gly	Ser	Ser	Pro		
103			110					115					120					
104																		
105	CCG	GTC	CTG	TGC	TCC	AAC	TCT	TCT	AGC	CTG	GGC	TCC	AGC	ACC	CCG	ACC		613
106	Pro	Val	Leu	Cys	Ser	Asn	Ser	Ser	Ser	Leu	Gly	Ser	Ser	Thr	Pro	Thr		
107		125					130					135						
108																		
109	GGA	GCC	GCG	TGC	GCA	CCA	AGG	GAT	TAT	GGC	CGT	CAA	GCG	CTG	TCA	CCC		661
110	Gly	Ala	Ala	Cys	Ala	Pro	Arg	Asp	Tyr	Gly	Arg	Gln	Ala	Leu	Ser	Pro		
111	140					145					150					155		
112																		
113	GCA	GAA	GTG	GAG	AAG	AGA	AGT	GGC	AGC	AAA	AGA	AAA	AGC	GAC	AGT	TCA		709
114	Ala	Glu	Val	Glu	Lys	Arg	Ser	Gly	Ser	Lys	Arg	Lys	Ser	Asp	Ser	Ser		
115					160					165					170			
116																		
117	GAT	TCC	CAG	GAA	GGA	AAT	TAC	AAG	TCA	GAA	GTG	AAC	AGC	AAA	CCT	AGG		757
118	Asp	Ser	Gln	Glu	Gly	Asn	Tyr	Lys	Ser	Glu	Val	Asn	Ser	Lys	Pro	Arg		
119			175					180						185				
120																		
121	AGG	GAA	AGA	ACA	GCT	TTC	ACC	AAA	GAG	CAA	ATC	AGA	GAA	CTT	GAG	GCA		805
122	Arg	Glu	Arg	Thr	Ala	Phe	Thr	Lys	Glu	Gln	Ile	Arg	Glu	Leu	Glu	Ala		
123			190					195					200					
124																		
125	GAG	TTC	GCC	CAT	CAT	AAC	TAT	CTG	ACC	AGA	CTG	AGA	AGA	TAT	GAG	ATA		853
126	Glu	Phe	Ala	His	His	Asn	Tyr	Leu	Thr	Arg	Leu	Arg	Arg	Tyr	Glu	Ile		
127		205					210					215						
128																		
129	GCG	GTG	AAC	CTA	GAC	CTC	ACT	GAA	AGA	CAG	GTG	AAA	GTG	TGG	TTC	CAG		901
130	Ala	Val	Asn	Leu	Asp	Leu	Thr	Glu	Arg	Gln	Val	Lys	Val	Trp	Phe	Gln		
131	220					225					230					235		
132																		
133	AAC	AGG	AGA	ATG	AAG	TGG	AAG	CGG	GTC	AAG	GGG	GGA	CAA	CAA	GGA	GCT		949
134	Asn	Arg	Arg	Met	Lys	Trp	Lys	Arg	Val	Lys	Gly	Gly	Gln	Gln	Gly	Ala		
135					240					245					250			
136																		
137	GCA	GCC	CGA	GAA	AAG	GAA	CTG	GTG	AAT	GTG	AAA	AAG	GGA	ACA	CTT	CTT		997
138	Ala																	

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153 ATTGTGATGG CAAATCTCAC CCAAACATCG TTTACATGGC AGATGACTGT GGCAGTGTG 1205
154
155 CTTAATATAA TTAAACGCAG GCATCTCAAG TCTGTTTCTC ATGATTGATA GAAGGTTTAC 1265
156
157 ACTAAGTGCC TCTTATTGAA GATGCTTCCA CAGTGAAATT GGAGAAAGTG AACATATCTA 1325
158
159 AATATACTTG TTCCTTATAT GACAGAGAGG GAGATGAATG TTTGCTTTGG CTTGCACTGA 1385
160
161 AAATTAAATT GCTACCAAGA GCAAACCTCG TAAGACATTT TGA CTCAAGT TGTCTCCAGA 1445
162
163 GTGAAGATGT TATAGAAATG CTTTGAACAT TCCAGTTGTA CCAGGTCATG TGTGTGACAC 1505
164
165 TGGGCAGGTA TTTGCTTTTG CTTGCACTGA AACTTAAACT GCTATCAAGT TAACCCATGA 1565
166
167 AATAGTTTAT CTTGAACAGC CACAGTGCCT GAAATCACCA AGTGGATATA AAATGAACTG 1625
168
169 AAATTCTGTA TATATTACTC CTAAGTCATT TTCCTGTCTT CACTAATTTT AGCAAATGCA 1685
170
171 TTCATATTAG CTGATGAAAA TAGGCTTTCC CGTGGACAAA TGCAGCCAGC TTCTTGTATT 1745
172
173 TTTATACATT TTTTGTGTCAG TCAGAGACAT CAGTATGTGC TTA CTGTGT TCAAGTAGAG 1805
174
175 GAAATGCAGT AGAGTCTGAT AGGACATATT CTTGGTACCA CAGACAAAAC AAATCTTCTG 1865
176
177 TTGCATTGAC TATCAACTGC TGCAGATACA TTAGAGAACA CACCTAGCCC CCCTCCAGCC 1925
178
179 TCCCTCTGTT ATCGCTCGAA GACATTAGCG TCATAGGCAA GTAGTTACCT TGCCAAATGA 1985
180
181 GTCTTGTGTG GCAGATGTCT GATTTTGTAT CTTTAACTG TTAATGGTAT GTGTCTGCTT 2045
182
183 CAGTTAACAG GGAAAAAGAT TTCTTCCTCA TTGTTTATGA TACAAAACCC AAGTGCCAAA 2105
184
185 CAAAGCTAGT TCTTCAAGGG ATAGATGAGA AACTGAATGT CTGACAAGTA GACTCAGCGA 2165
186
187 AAATACATTA TTTTTCAGAG GCTGTGTATT CATGCAGTAC AAGTCCTTGT ATTTTGTAAA 2225
188
189 AAAAAAAGTT AAATAAATG 2244

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

203 Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser Pro His Ala Thr Ala
204 1 5 10 15
205

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206	Gln	Gly	Leu	His	Pro	Phe	Ser	Gln	Ser	Ser	Leu	Ala	Leu	His	Gly	Arg
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208																
209	Ser	Asp	His	Met	Ser	Tyr	Pro	Glu	Leu	Ser	Thr	Ser	Ser	Ser	Ser	Cys
210			35					40					45			
211																
212	Ile	Ile	Ala	Gly	Tyr	Pro	Asn	Glu	Glu	Gly	Met	Phe	Ala	Ser	Gln	His
213			50				55					60				
214																
215	His	Arg	Gly	His	His	His	His	His	His	His	His	His	His	His	His	Gln
216		65					70				75					80
217																
218	Gln	Gln	Gln	His	Gln	Ala	Leu	Gln	Ser	Asn	Trp	His	Leu	Pro	Gln	Met
219					85					90					95	
220																
221	Ser	Ser	Pro	Pro	Ser	Ala	Ala	Arg	His	Ser	Leu	Cys	Leu	Gln	Pro	Asp
222				100					105					110		
223																
224	Ser	Gly	Gly	Pro	Pro	Glu	Leu	Gly	Ser	Ser	Pro	Pro	Val	Leu	Cys	Ser
225			115					120					125			
226																
227	Asn	Ser	Ser	Ser	Leu	Gly	Ser	Ser	Thr	Pro	Thr	Gly	Ala	Ala	Cys	Ala
228		130					135					140				
229																
230	Pro	Arg	Asp	Tyr	Gly	Arg	Gln	Ala	Leu	Ser	Pro	Ala	Glu	Val	Glu	Lys
231		145				150					155					160
232																
233	Arg	Ser	Gly	Ser	Lys	Arg	Lys	Ser	Asp	Ser	Ser	Asp	Ser	Gln	Glu	Gly
234					165				170						175	
235																
236	Asn	Tyr	Lys	Ser	Glu	Val	Asn	Ser	Lys	Pro	Arg	Arg	Glu	Arg	Thr	Ala
237				180					185					190		
238																
239	Phe	Thr	Lys	Glu	Gln	Ile	Arg	Glu	Leu	Glu	Ala	Glu	Phe	Ala	His	His
240			195					200					205			
241																
242	Asn	Tyr	Leu	Thr	Arg	Leu	Arg	Arg	Tyr	Glu	Ile	Ala	Val	Asn	Leu	Asp
243		210					215					220				
244																
245	Leu	Thr	Glu	Arg	Gln	Val	Lys	Val	Trp	Phe	Gln	Asn	Arg	Arg	Met	Lys
246		225				230					235					240
247																
248	Trp	Lys	Arg	Val	Lys	Gly	Gly	Gln	Gln	Gly	Ala	Ala	Ala	Arg	Glu	Lys
249					245					250					255	
250																
251	Glu	Leu	Val	Asn	Val	Lys	Lys	Gly	Thr	Leu	Leu	Pro	Ser	Glu	Leu	Ser
252				260					265					270		
253																
254	Gly	Ile	Gly	Ala	Ala	Thr	Leu	Gln	Gln	Thr	Gly	Asp	Ser	Leu	Ala	Asn
255			275					280					285			
256																
257	Asp	Asp	Ser	Arg	Asp	Ser	Asp	His	Ser	Ser	Glu	His	Ala	His	Leu	
258		290					295					300				

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/10/784,513

DATE: 03/20/2006
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INPUT SET: S30786.raw

Line	Error	Original Text
32	Wrong Classification	(C) CLASSIFICATION:435